

Fig. 1A

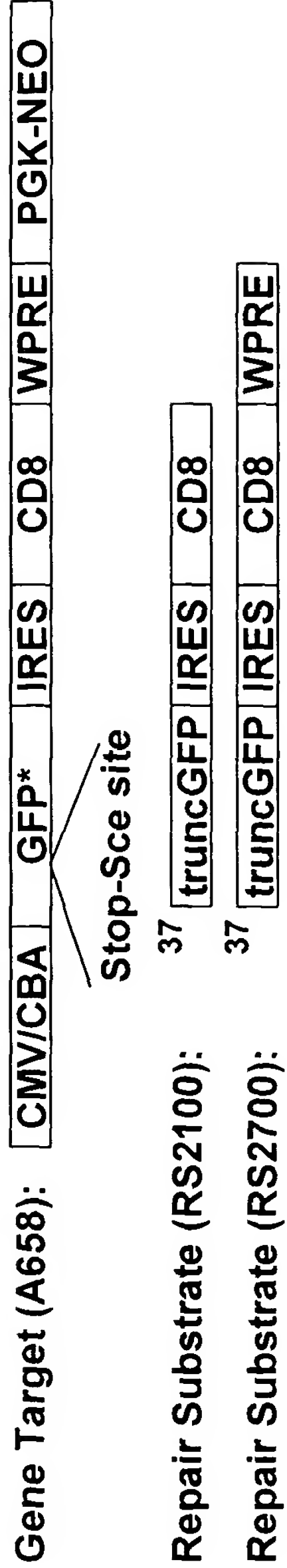


Fig. 1B

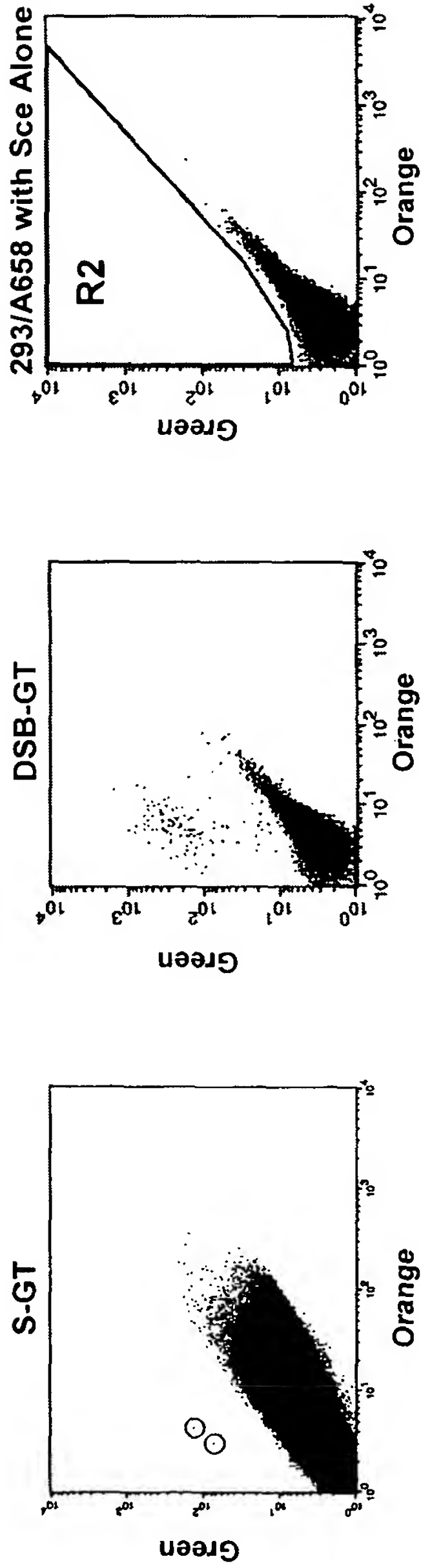


Fig. 1C

Gene Target		<u>1bp insertion</u>		<u>7 bp insertion</u>		<u>35 bp insertion (A658)</u>		<u>66 bp insertion (QQR8)</u>		Fold Stimulation By Sce Induced DSB	
Sce		No		No		Yes		Yes			
Events/ 10 ⁶ cells		29.5 +/- 13.0		1.5 +/- 1.1		0.71 +/- 0.27		1600 +/- 500		1900 +/- 250	
Rate		2.9 x 10 ⁻⁵		1.5 x 10 ⁻⁶		7.1 x 10 ⁻⁷		1.6 x 10 ⁻³		1.9 x 10 ⁻³	
										>2000	

Fig. 1D

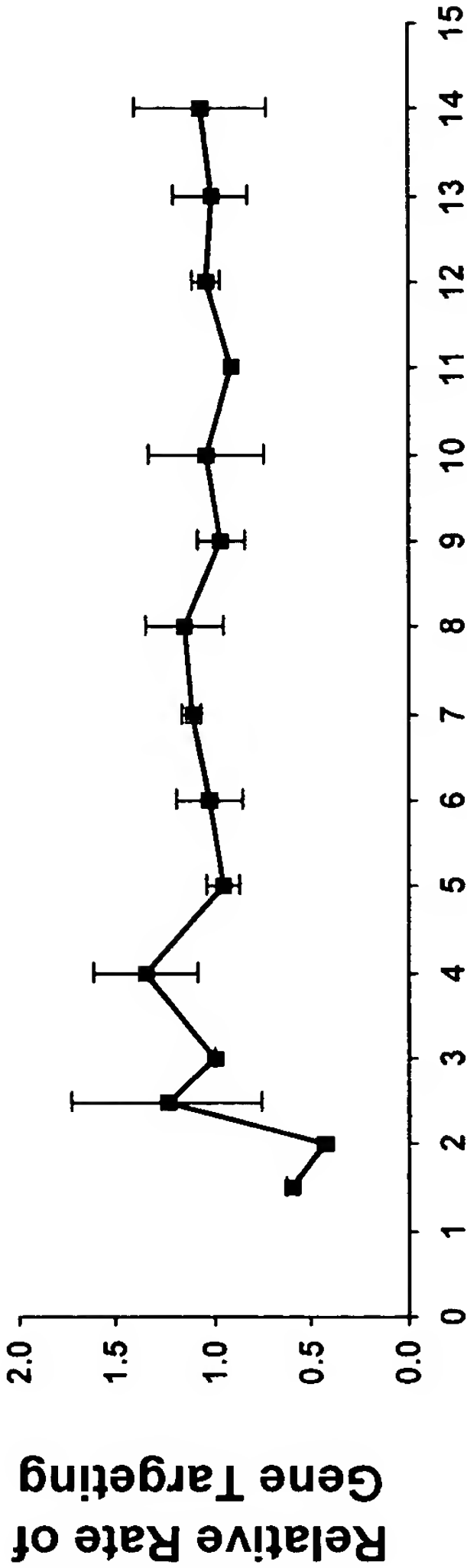


Fig. 2A

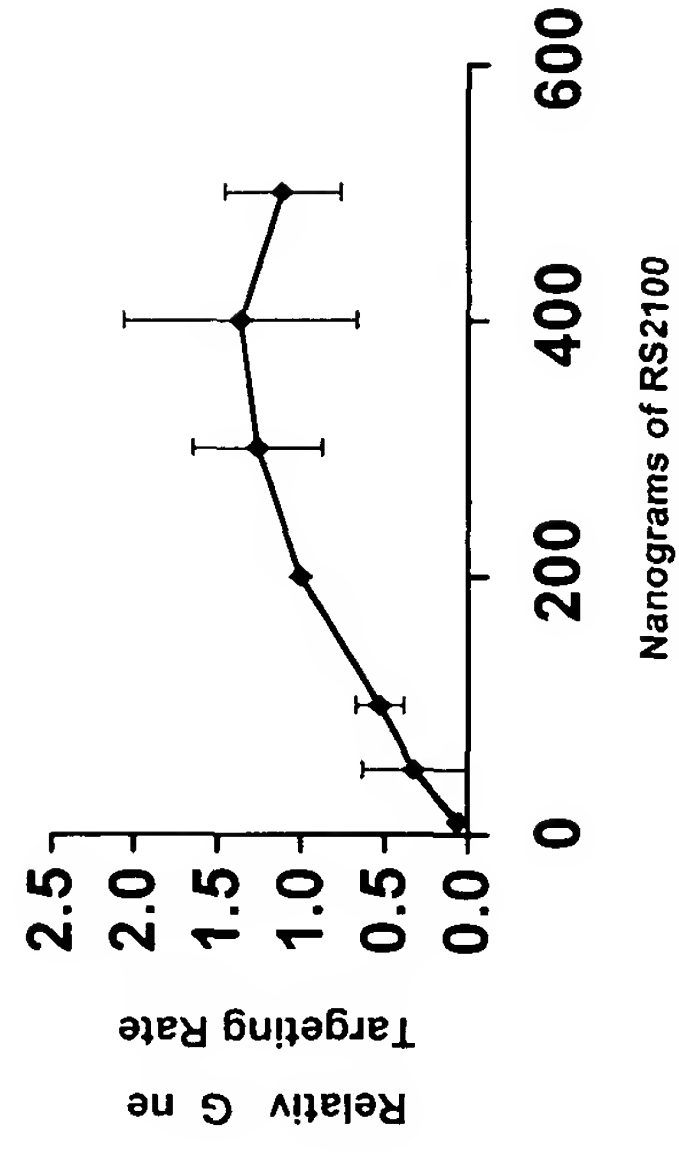


Fig. 2B

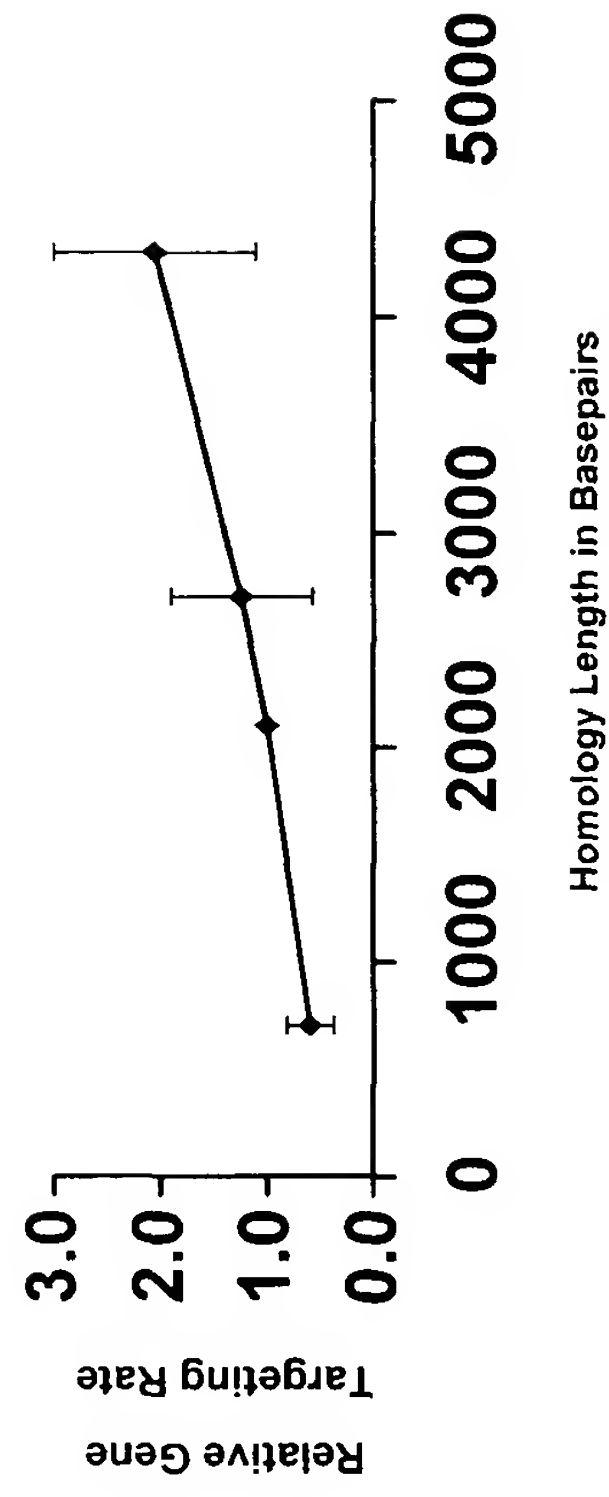


Fig. 2C

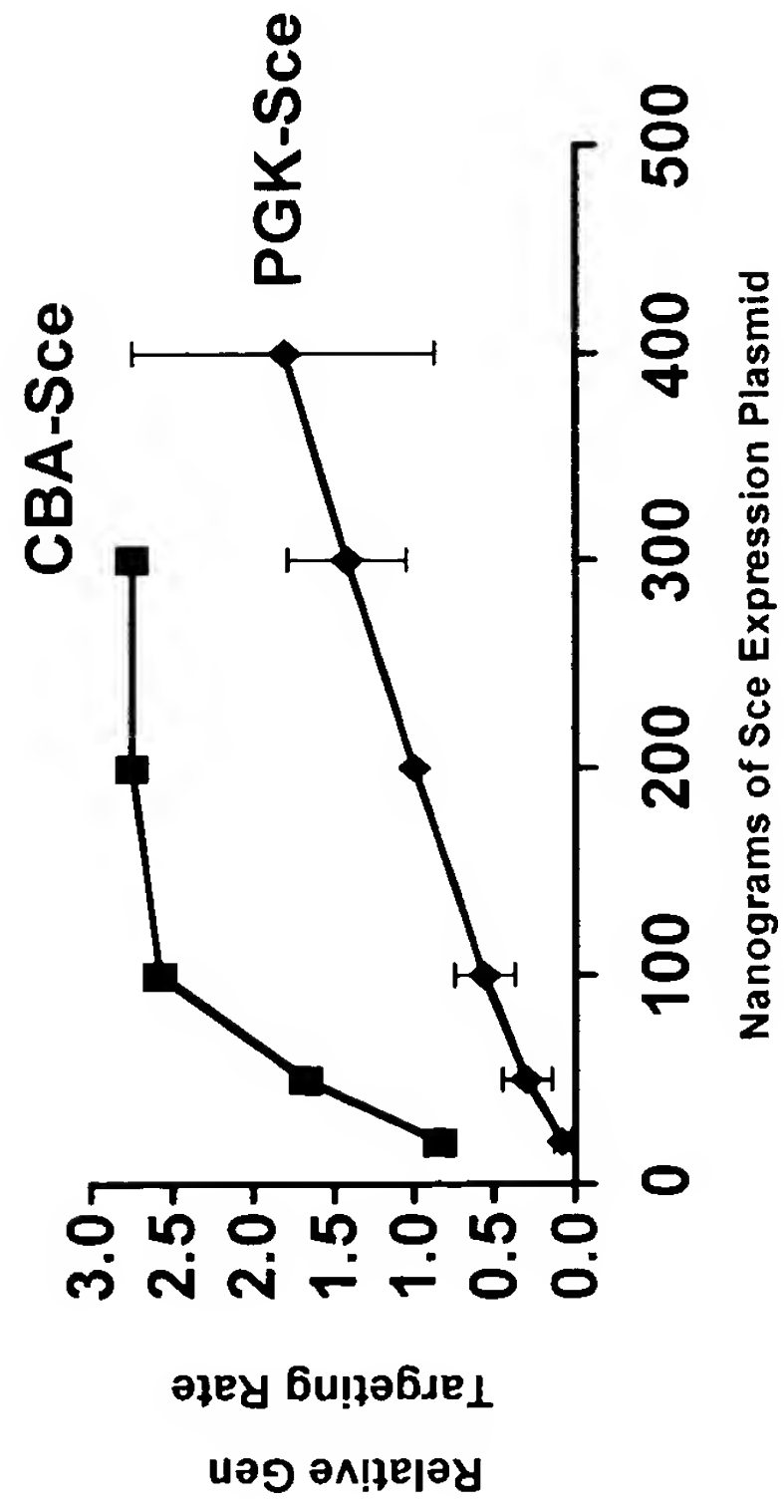


Fig. 2D

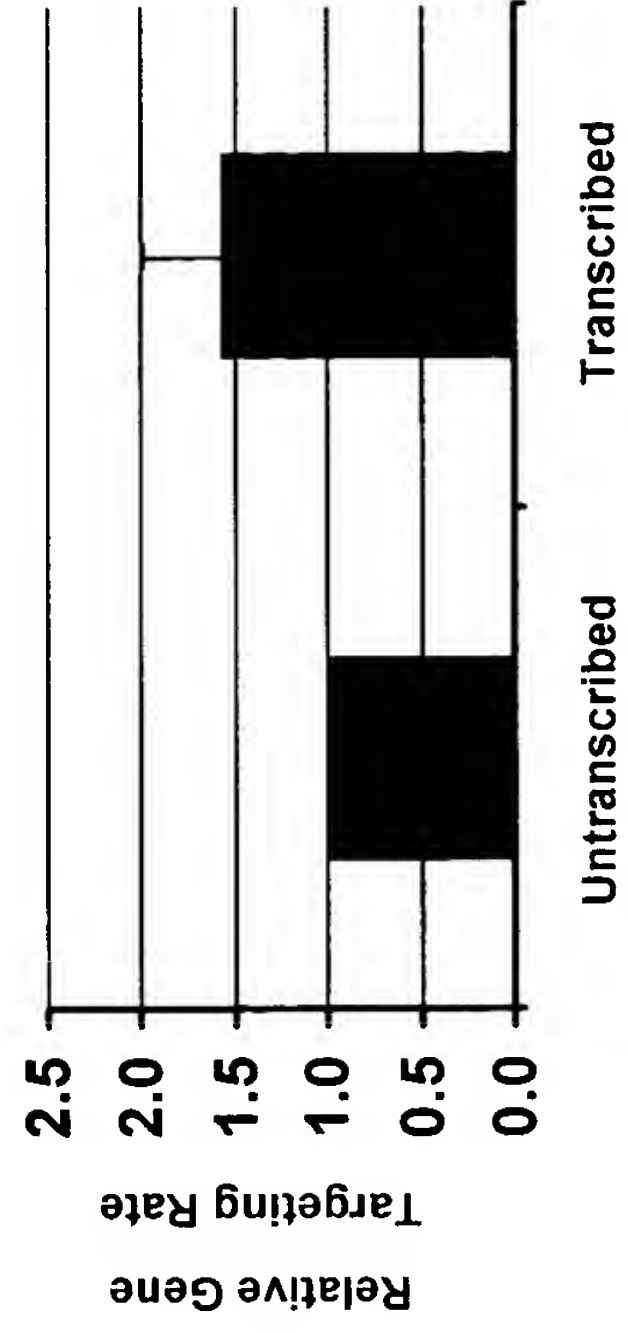


Fig. 2E

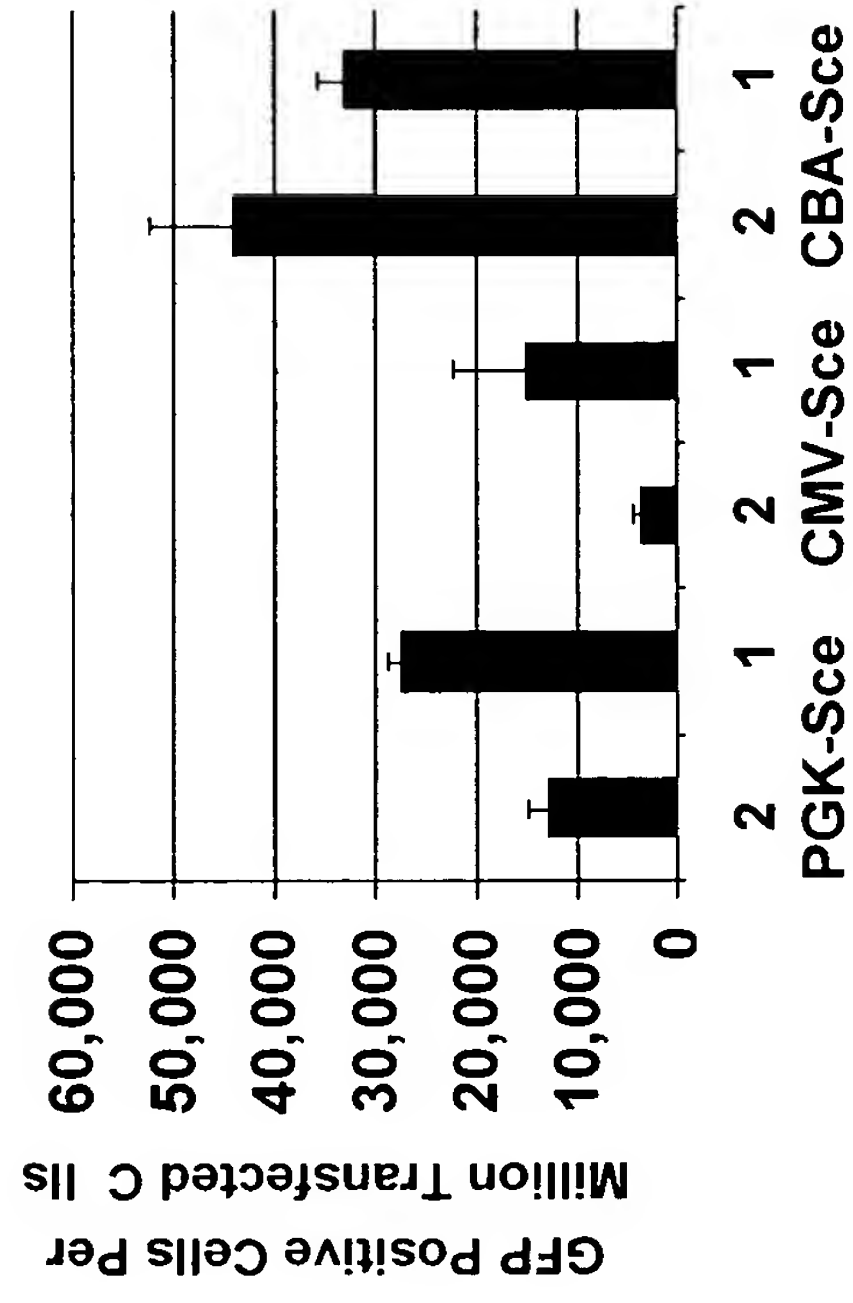


Fig. 3A

Targets:			Chimeric Nucleases:		
QQR8:	5' GFP	Stop QQR Site 8	Stop QQR Site 8	CMV	ATG N QQR L18 Nuclease
QQR6:	5' GFP	Stop QQR Site 6	Stop QQR Site 6	CMV	ATG N QQR L0 Nuclease
QQRZif6:	5' GFP	Stop QQR Site 6	Stop QQR Site 6	CMV	ATG N Zif L3 Nuclease

Fig. 3B

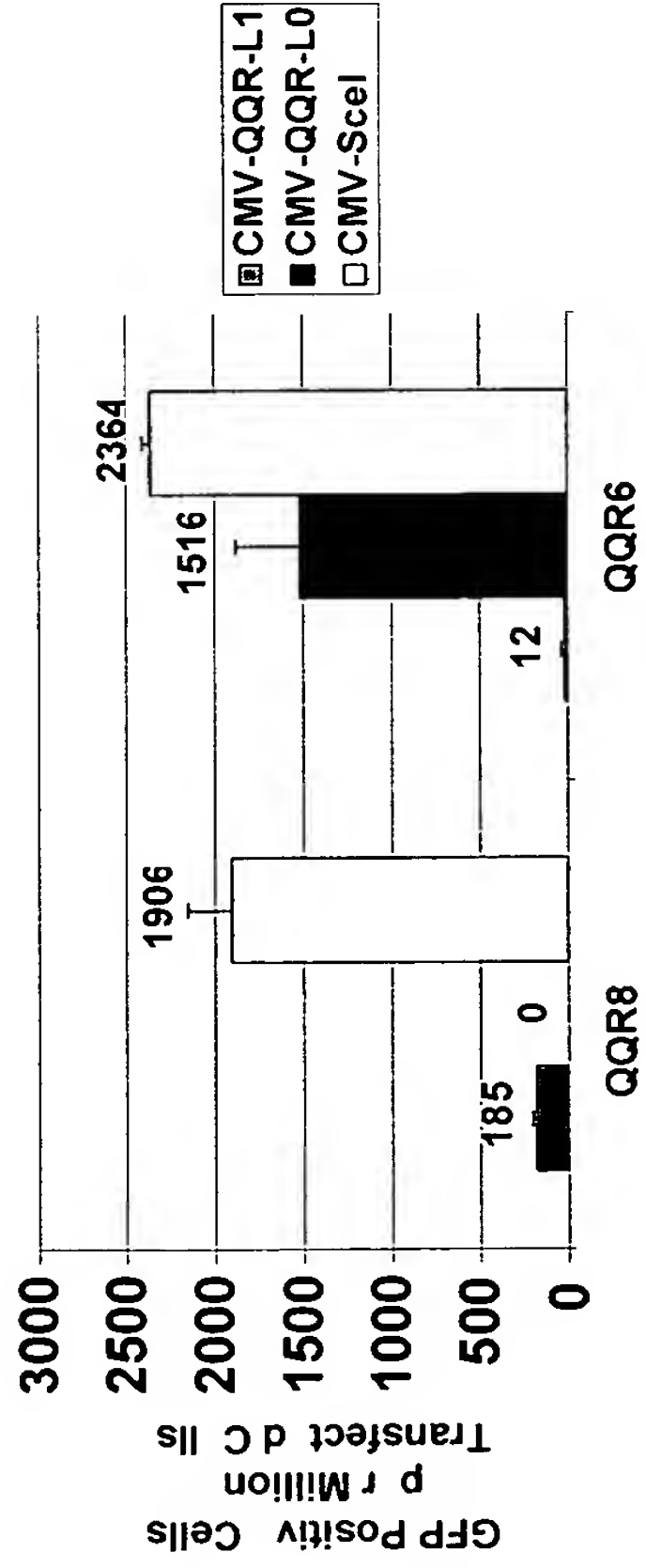


Fig. 3C

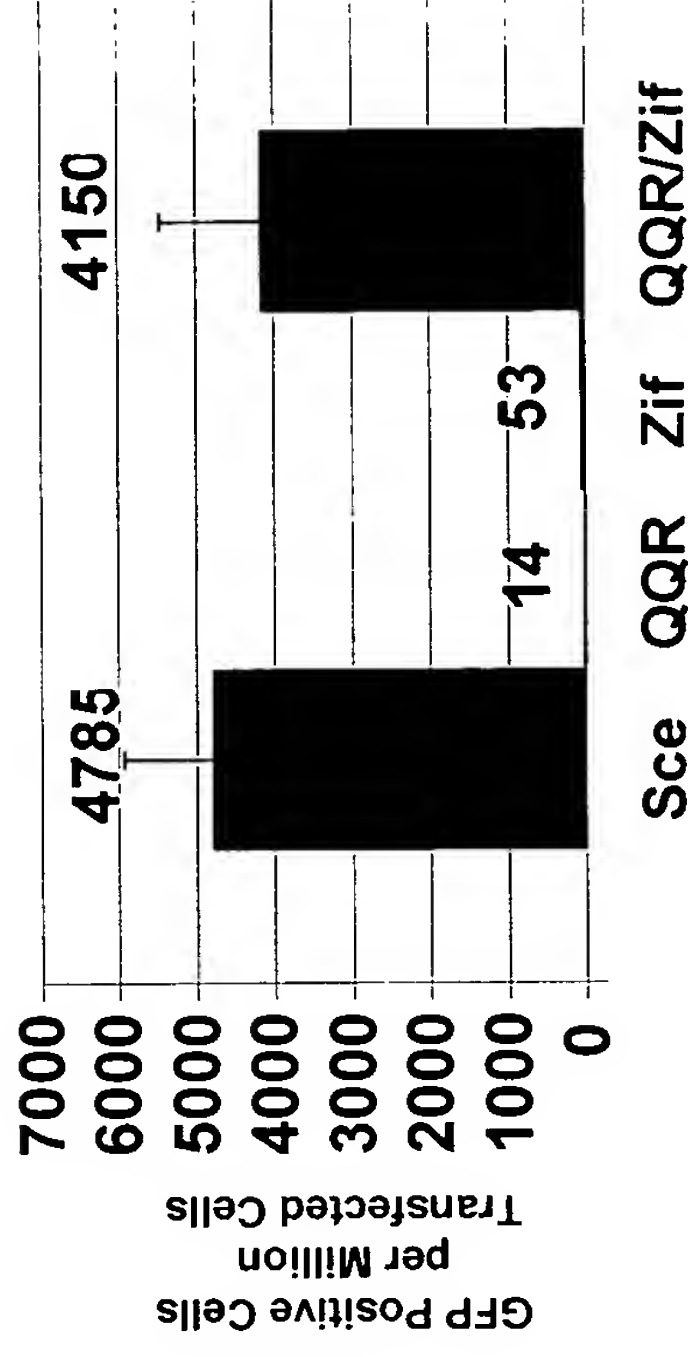


Fig. 3D

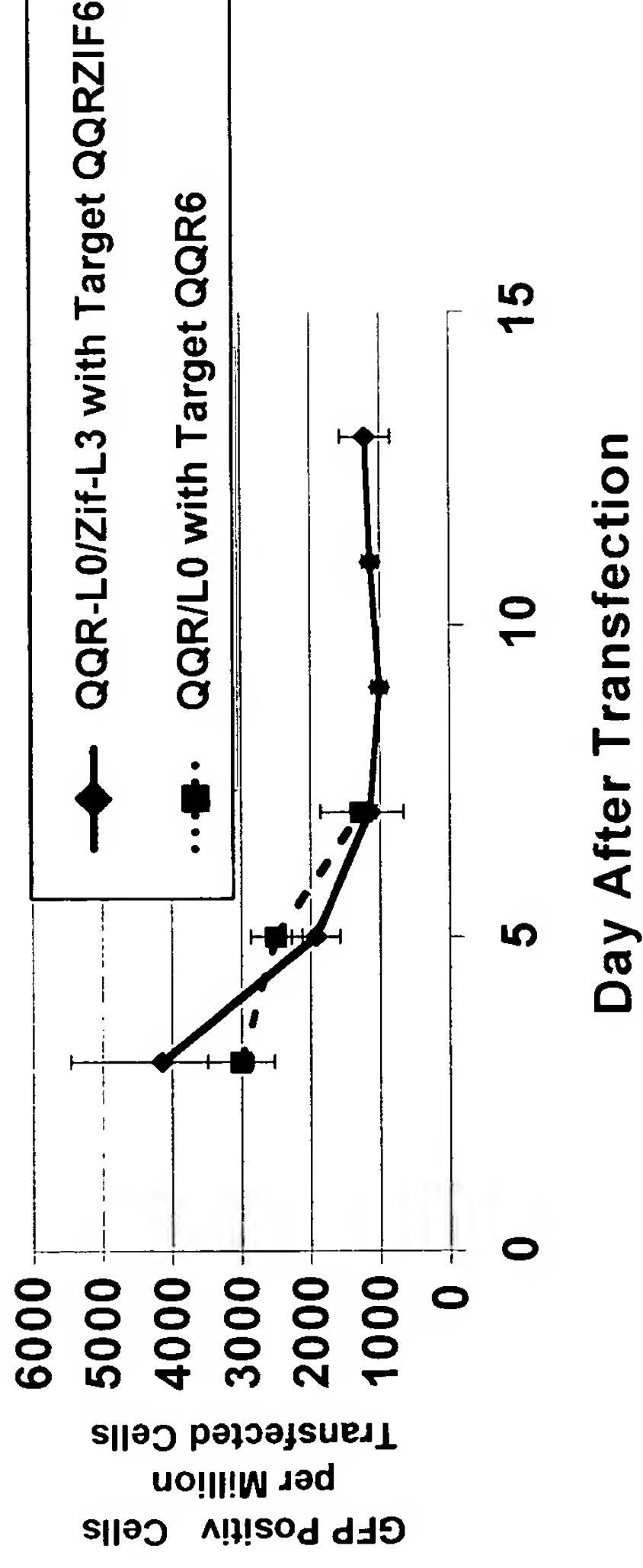


Fig. 4

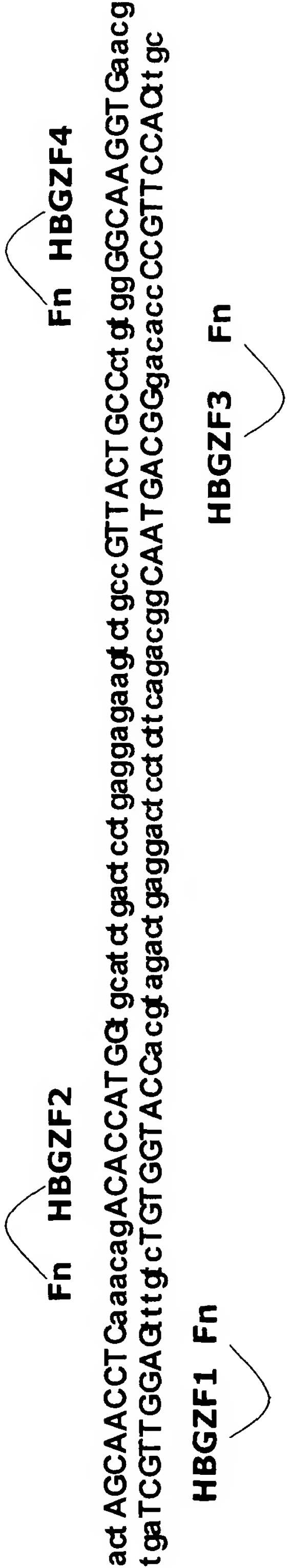


Fig. 5

Design of HBGZF1

Target Binding Site: 5' GAG GTT GCT 3'
F3 F2 F1

-1 1 2 3 4 5 6
B3 B2 B1

Finger 1:	GCT	Q S S D L T R*
		T S G E L V R
Finger 2:	GTT	T S G A L T R*
		T S G S L T R
Finger 3:	GAG	R S D N L T R*
		R S D N L V R

Structure of CMV-HBGZF1



ATG-NLS-FLAG-Finger 1(QSSDLTR)-Finger2(TSGALTR)-Finger3(RSDNLTR)-Fn

Fig. 6

Gene Targeting with HBGZF1

Target: GFP-St op- AGCAACCTQ d aga GCGT GGGCG- SceSt e- GFP
TCGTTGGAGagatd CGCACCCCGC

Fn ZIF268

HBGZF1 Fn

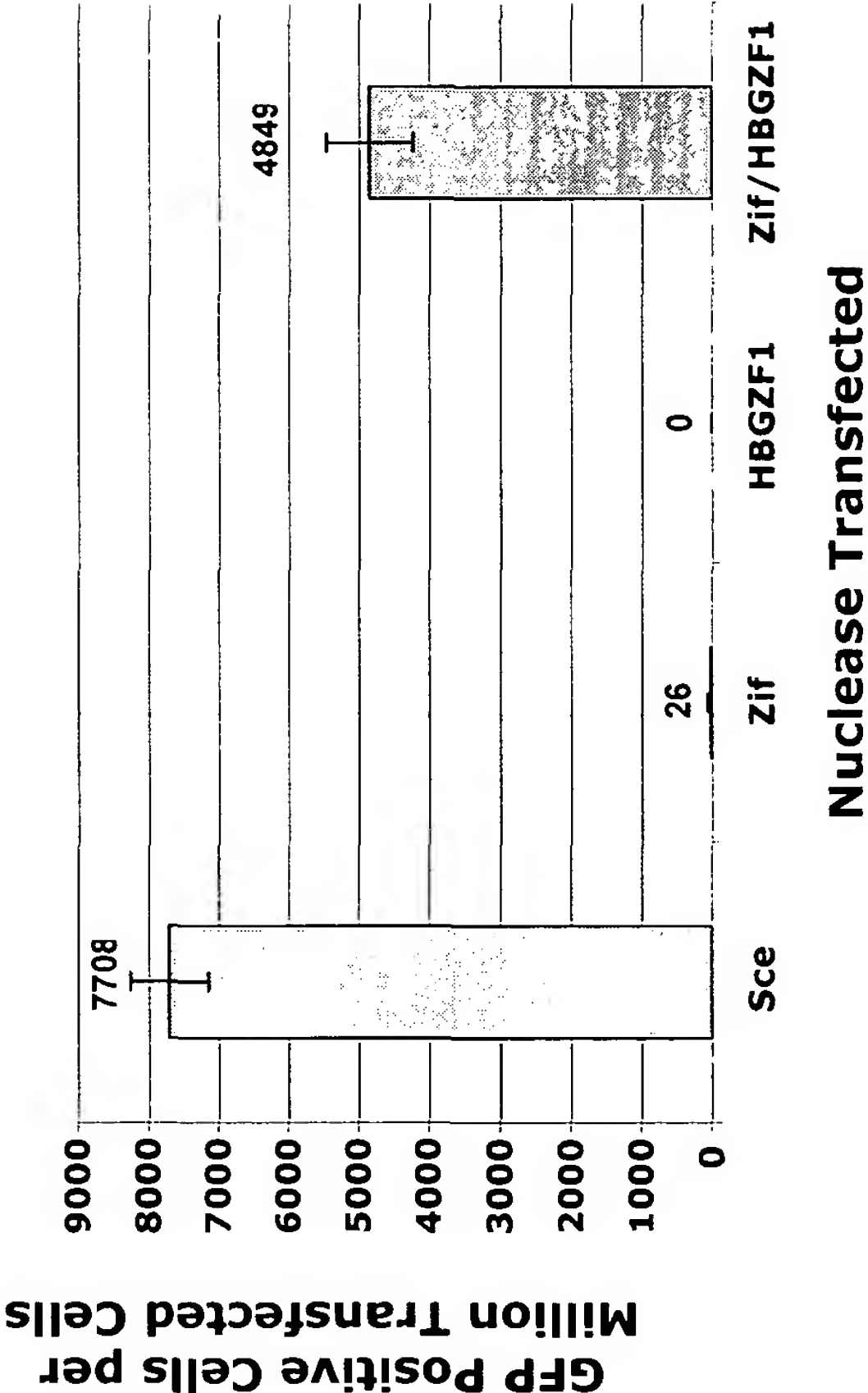


Fig. 7

Design of HBGZF4

Target Binding Site: 5' GGC AAG GTG 3'
F3 F2 F1

-1 1 2 3 4 5 6
B3 B2 B1

Finger 1: GTG R S D A L T R*
R S N S L T R

Finger 2: AAG R S D T L S N
R K D N L K N
R S S N L T Q

Finger 3: GGC D R S H L A R*
E S N H L T R
E R S K L A R
D P G H L V R

Structure of CMV-HBGZF1



Fig. 8

Gene Targeting with HBGZF4

Target: GFP-St op- CACCTTGCQ ct aga GCGT GGGCG- SceSite- GFP
GTGGAACGGagat ct CGCACCCGC

Fn ZIF268

HBGZF4 Fn

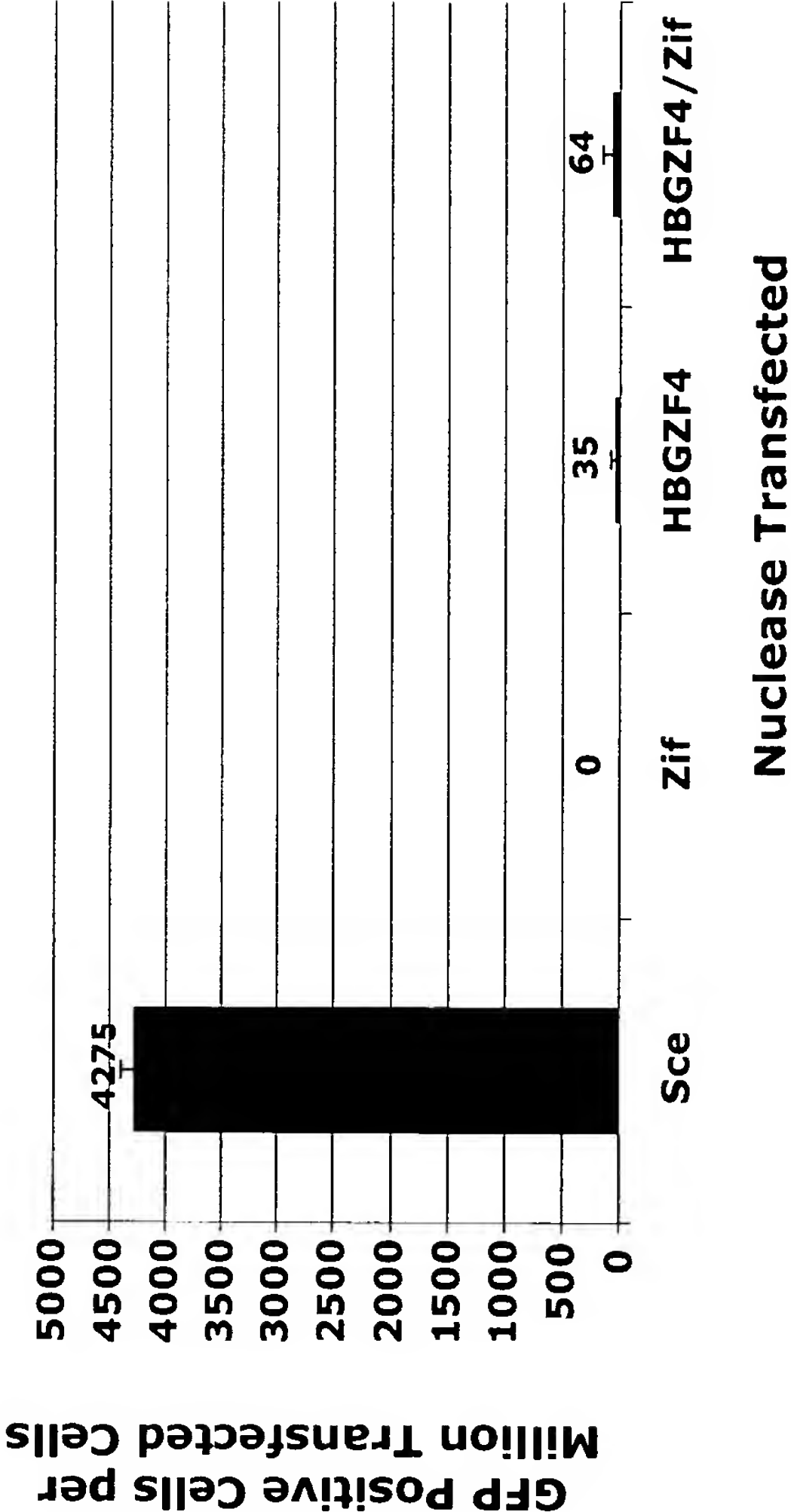


Fig. 9A

Human Common Gamma Chain Deficiency

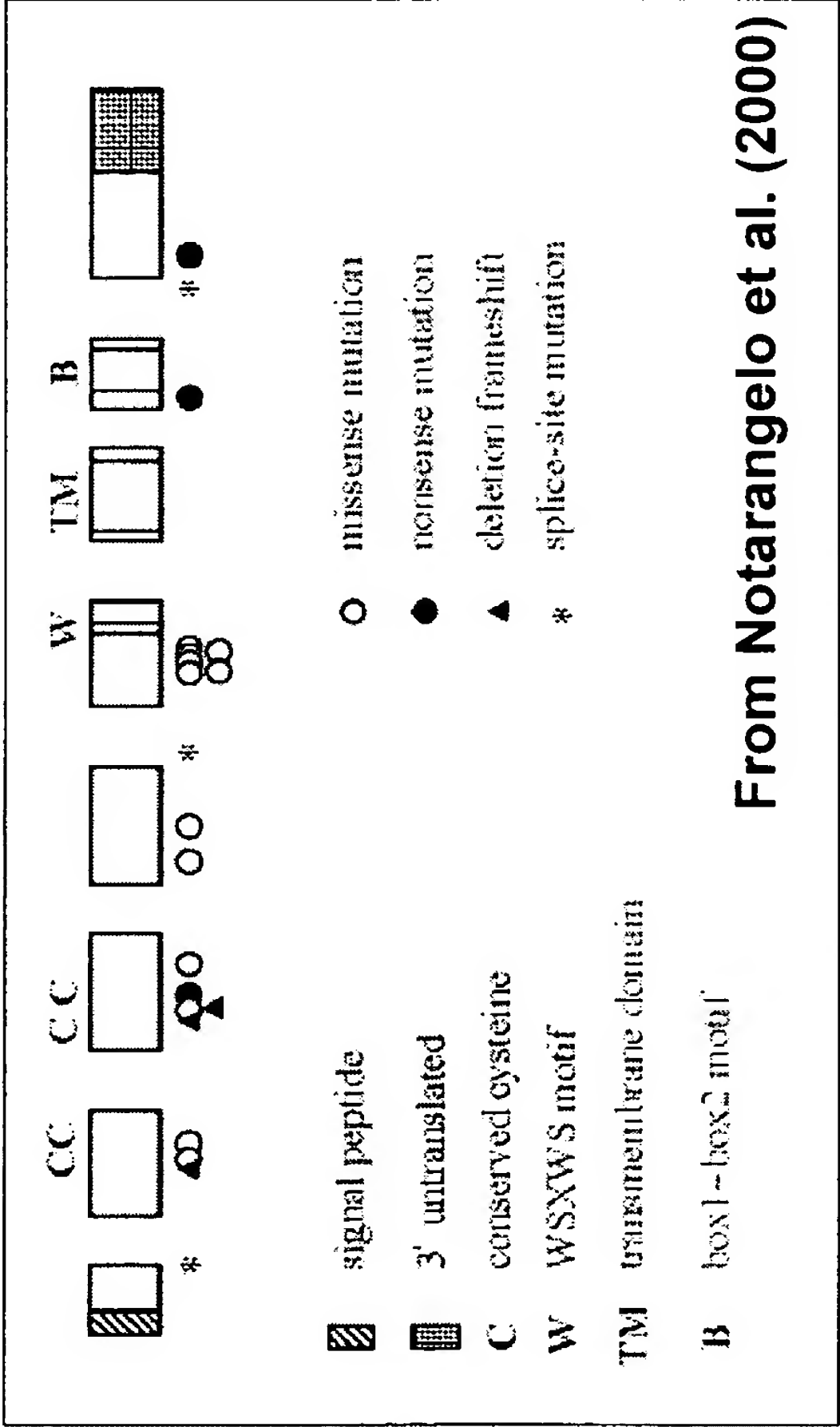


Fig. 9B

Exon 5

5' gaacaat cagt ggatt at agacat aagt t ct cctt gcct agt gt ggat gggcagaaacgct acacgttt cgt gtt
3' ctt gtt agt cacct aat at ct gt att caagaggaacggat cacacct acccgt dtt gcgat gt gcaaagcacaa
WSXWS motif HCGCZF2
cggagccgctttaaccact ct gt ggaagt gct cagcatt ggagt gaat ggagccaccaat ccact gggggagca
gcct cggcgaaatt ggggt gagacacctt cacgagt cgt aacct cacttacct cgggt ggggt aggt gacccct cgt
HCGCZF1
at act caaaagag 3'
t at gaagt ttt ct g 5'

Fig. 10

Design of HCGCZF2

Target Binding Site: 5' GGG GGA GCA 3'

F3 F2 F1

-1 1 2 3 4 5 6

B3 B2 B1

Finger 1: GCA Q S G S L T R
Q S G D L T R
Q S G D L T R
Q S N D L T R

Finger 2: GGA Q S G H L Q K
Q R A H L E R
Q S S H L T R

Finger 3: GGG R S D H L A R
R S D H L T R
R S S H L T R

Structure of CMV-HCGCZF2



ATG-NLS-FLAG-Finger 1(QSNDLTR)-Finger2(QSSHLTR)-Finger3(RSSHLTR)-Fn

Fig. 11

Gene Targeting with HCGCZF2

Target: GFP-St op-TGCTCCCCCQct aga GCGTGGGCG-SceSite-GFP

ACGAGGGGGagatct CGCACCCGC

Fn ZIF268

HCGCZF2 Fn

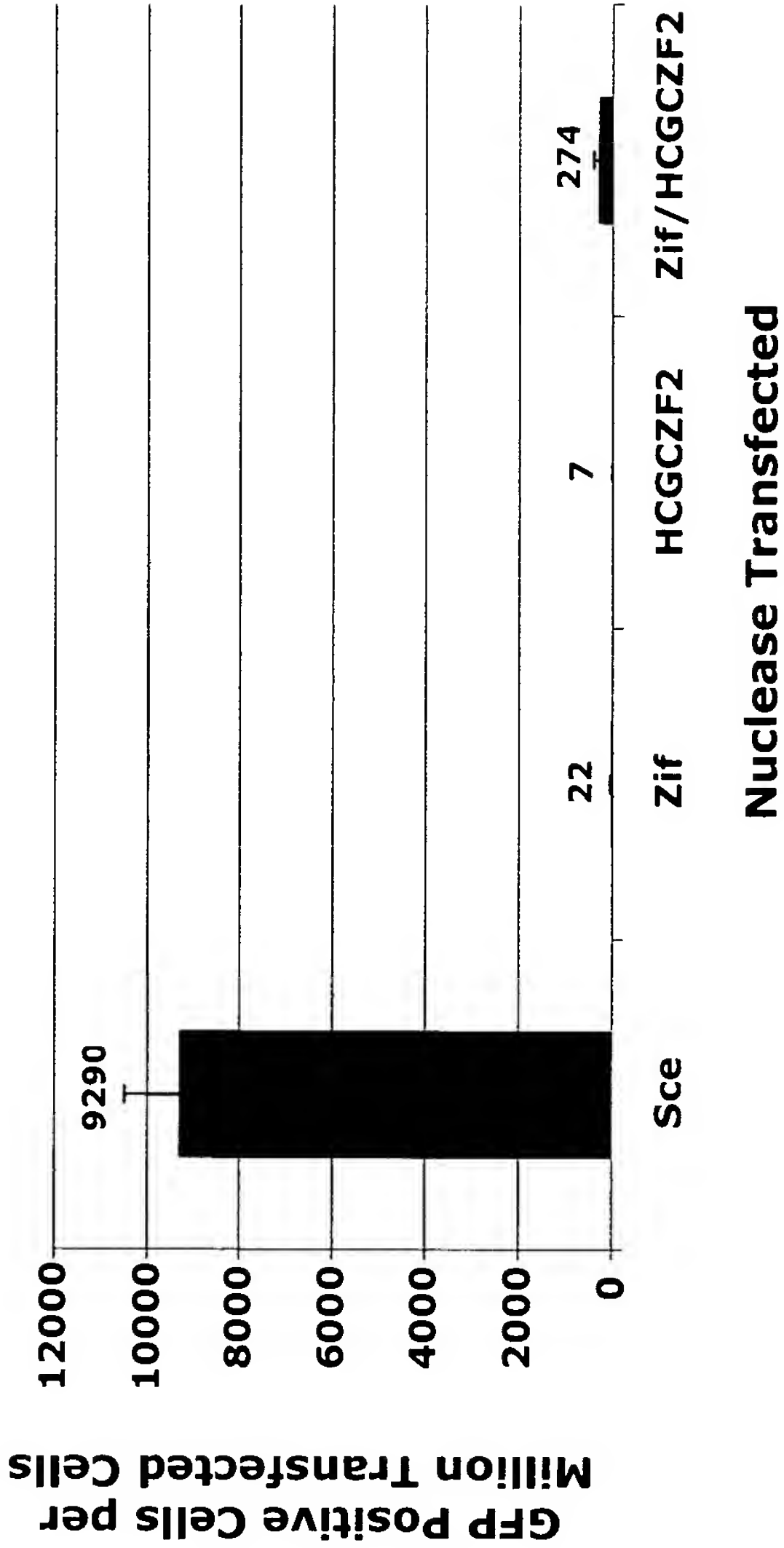


Fig. 12A

Fn  **GFPNC2**

5' acC at CttC ttc aag Gac Gac Ggc aac stop-Sce site tac

3' tgGtaGaaG aag ttc Cgc A g Ccg ttc

GFPNC1  **Fn**

Fig. 12B

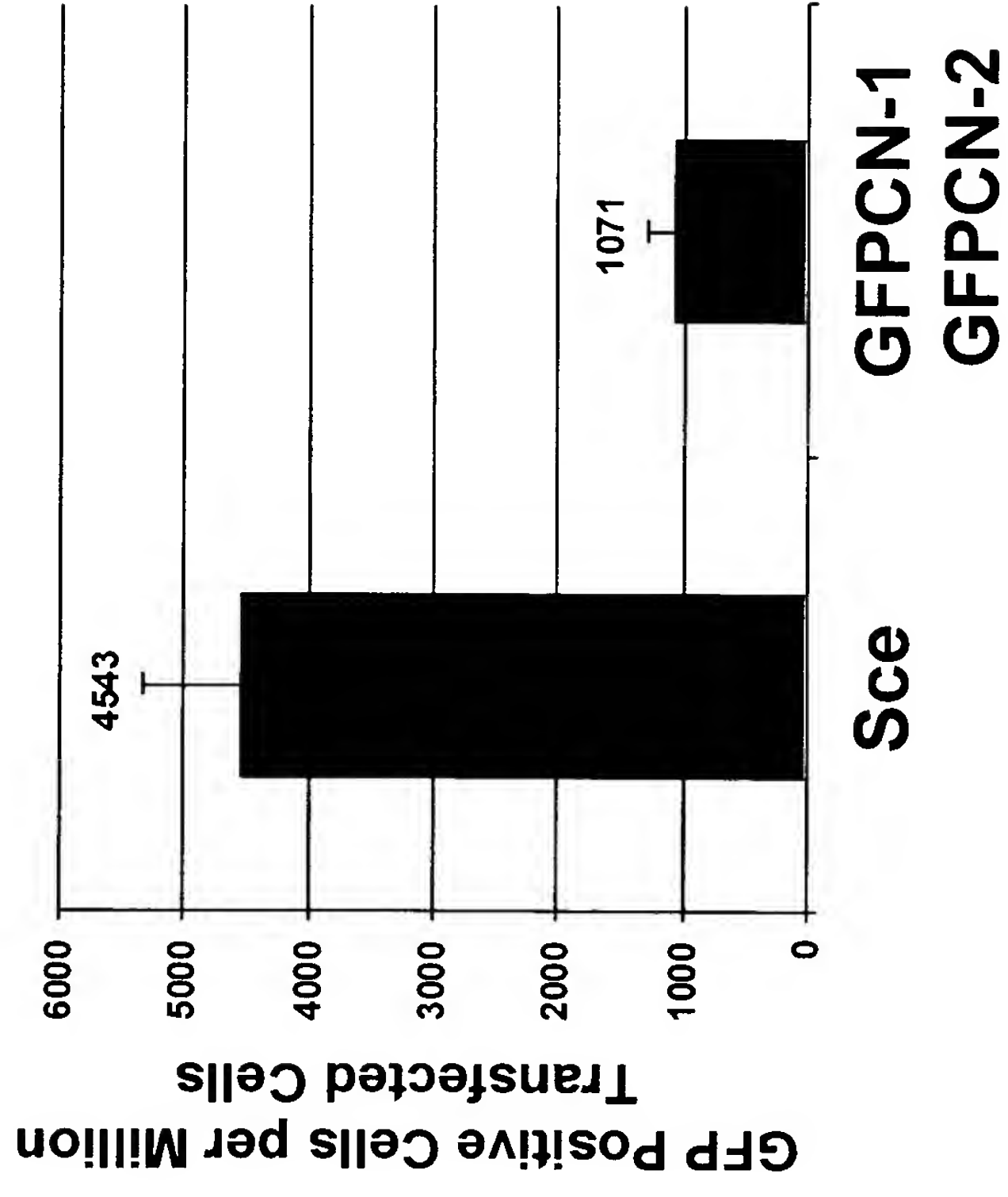


Fig. 13A

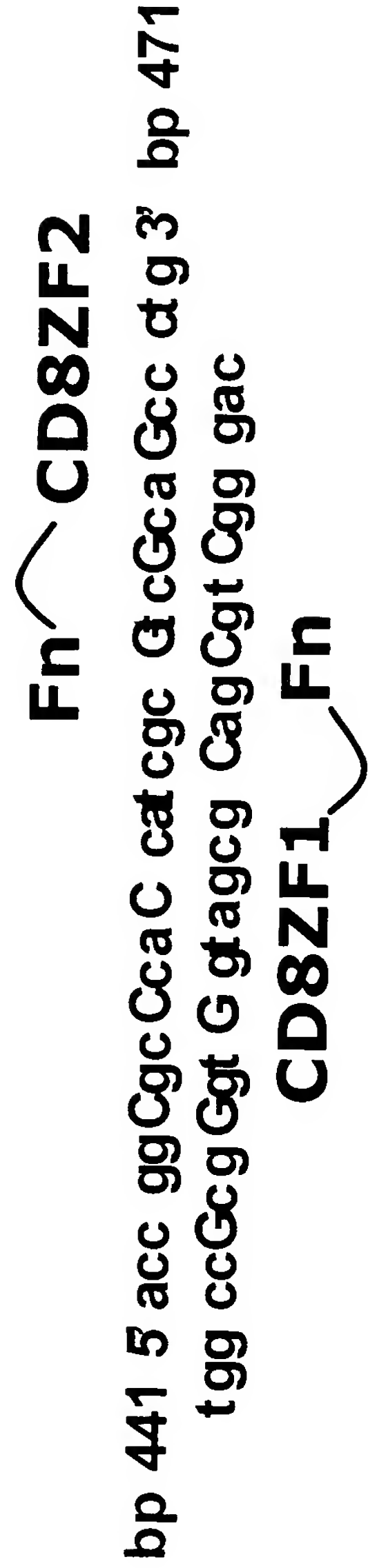


Fig. 13B

